

- SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: THE GENERAL HOSPITAL CORPORATION
FRUIT STREET
BOSTON, MA 02114
UNITED STATES OF AMERICA

APPLICANT/INVENTOR: de la Monte, Suzanne
Wands, Jack R.

(ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox P.L.L.C.
(B) STREET: 1100 New York Ave., Suite 600
(C) CITY: Washington
(D) STATE: DC
(E) COUNTRY: USA
(F) ZIP: 20005-3934

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To be assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 60/038,908
(B) FILING DATE: 26-FEB-1997

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Esmond, Robert W.
(B) REGISTRATION NUMBER: 32,893
(C) REFERENCE/DOCKET NUMBER: 0609.437PC01

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 202-371-2600
(B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1442 base pairs

09964666 . 092801

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS
(B) LOCATION: 15..1139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC	50
Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys	
1 5 10	
AAT GGC GCA ATC TCA GCT CAC CGC AAC CTC CGC CTC CCG GGT TCA AGC	98
Asn Gly Ala Ile Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser	
15 20 25	
GAT TCT CCT GCC TCA GCC TCC CCA GTA GCT GGG ATT ACA GGC ATG TGC	146
Asp Ser Pro Ala Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys	
30 35 40	
ACC CAC GCT CGG CTA ATT TTG TAT TTT TTT TTA GTA GAG ATG GAG TTT	194
Thr His Ala Arg Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe	
45 50 55 60	
CTC CAT GTT GGT CAG GCT GGT CTC GAA CTC CCG ACC TCA GAT GAT CCC	242
Leu His Val Gly Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro	
65 70 75	
TCC GTC TCG GCC TCC CAA AGT GCT AGA TAC AGG ACT GGC CAC CAT GCC	290
Ser Val Ser Ala Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala	
80 85 90	
CGG CTC TGC CTG GCT AAT TTT TGT GGT AGA AAC AGG GTT TCA CTG ATG	338
Arg Leu Cys Leu Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met	
95 100 105	
TGC CCA AGC TGG TCT CCT GAG CTC AAG CAG TCC ACC TGC CTC AGC CTC	386
Cys Pro Ser Trp Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu	
110 115 120	
CCA AAG TGC TGG GAT TAC AGG CGT GCA GCC GTG CCT GGC CTT TTT ATT	434
Pro Lys Cys Trp Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile	
125 130 135 140	
TTA TTT TTT TTA AGA CAC AGG TGT CCC ACT CTT ACC CAG GAT GAA GTG	482
Leu Phe Phe Leu Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val	
145 150 155	
CAG TGG TGT GAT CAC AGC TCA CTG CAG CCT TCA ACT CCT GAG ATC AAG	530
Gln Trp Cys Asp His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys	

09964566-092801

	160		165		170	
CAT CCT CCT GCC TCA GCC TCC CAA GTA GCT GGG ACC AAA GAC ATG CAC						578
His Pro Pro Ala Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His	175		180		185	
CAC TAC ACC TGG CTA ATT TTT ATT TTT ATT TTT AAT TTT TTG AGA CAG						626
His Tyr Thr Trp Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln	190		195		200	
AGT CTC AAC TCT GTC ACC CAG GCT GGA GTG CAG TGG CGC AAT CTT GGC						674
Ser Leu Asn Ser Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly	205		210		215	220
TCA CTG CAA CCT CTG CCT CCC GGG TTC AAG TTA TTC TCC TGC CCC AGC						722
Ser Leu Gln Pro Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser	225			230		235
CTC CTG AGT AGC TGG GAC TAC AGG CGC CCA CCA CGC CTA GCT AAT TTT						770
Leu Leu Ser Ser Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe	240		245		250	
TTT GTA TTT TTA GTA GAG ATG GGG TTC ACC ATG TTC GCC AGG TTG ATC						818
Phe Val Phe Leu Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile	255		260		265	
TTG ATC TCT GGA CCT TGT GAT CTG CCT GCC TCG GCC TCC CAA AGT GCT						866
Leu Ile Ser Gly Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala	270		275		280	
GGG ATT ACA GGC GTG AGC CAC CAC GCC CGG CTT ATT TTT AAT TTT TGT						914
Gly Ile Thr Gly Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys	285		290		295	300
TTG TTT GAA ATG GAA TCT CAC TCT GTT ACC CAG GCT GGA GTG CAA TGG						962
Leu Phe Glu Met Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp	305		310		315	
CCA AAT CTC GGC TCA CTG CAA CCT CTG CCT CCC GGG CTC AAG CGA TTC						1010
Pro Asn Leu Gly Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe	320		325		330	
TCC TGT CTC AGC CTC CCA AGC AGC TGG GAT TAC GGG CAC CTG CCA CCA						1058
Ser Cys Leu Ser Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro	335		340		345	
CAC CCC GCT AAT TTT TGT ATT TTC ATT AGA GGC GGG GTT TCA CCA TAT						1106
His Pro Ala Asn Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr	350		355		360	
TTG TCA GGC TGG TCT CAA ACT CCT GAC CTC AGG TGACCCACCT GCCTCAGCCT						1159
Leu Ser Gly Trp Ser Gln Thr Pro Asp Leu Arg	365		370		375	
TCCAAAGTGC TGGGATTACA GGC GTGAGCC ACCTCACCCA GCCGGCTAAT TTAGATAAAA						1219

09964666-092801

AAATATGTAG CAATGGGGGG TCTTGCTATG TTGCCCAGGC TGGTCTCAAA CTTCTGGCTT 1279
 CATGCAATCC TTCCAAATGA GCCACAACAC CCAGCCAGTC ACATTTTTTA AACAGTTACA 1339
 TCTTTATTTT AGTATACTAG AAAGTAATAC AATAAACATG TCAAACCTGC AAATTCAGTA 1399
 GTAACAGAGT TCTTTTATAA CTTTTAAACA AAGCTTTAGA GCA 1442

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys Asn Gly Ala Ile
 1 5 10 15
 Ser Ala His Arg Asn Leu Arg Leu Pro Gly Ser Ser Asp Ser Pro Ala
 20 25 30
 Ser Ala Ser Pro Val Ala Gly Ile Thr Gly Met Cys Thr His Ala Arg
 35 40 45
 Leu Ile Leu Tyr Phe Phe Leu Val Glu Met Glu Phe Leu His Val Gly
 50 55 60
 Gln Ala Gly Leu Glu Leu Pro Thr Ser Asp Asp Pro Ser Val Ser Ala
 65 70 75 80
 Ser Gln Ser Ala Arg Tyr Arg Thr Gly His His Ala Arg Leu Cys Leu
 85 90 95
 Ala Asn Phe Cys Gly Arg Asn Arg Val Ser Leu Met Cys Pro Ser Trp
 100 105 110
 Ser Pro Glu Leu Lys Gln Ser Thr Cys Leu Ser Leu Pro Lys Cys Trp
 115 120 125
 Asp Tyr Arg Arg Ala Ala Val Pro Gly Leu Phe Ile Leu Phe Phe Leu
 130 135 140
 Arg His Arg Cys Pro Thr Leu Thr Gln Asp Glu Val Gln Trp Cys Asp
 145 150 155 160
 His Ser Ser Leu Gln Pro Ser Thr Pro Glu Ile Lys His Pro Pro Ala
 165 170 175
 Ser Ala Ser Gln Val Ala Gly Thr Lys Asp Met His His Tyr Thr Trp
 180 185 190

09964566-092801

Leu Ile Phe Ile Phe Ile Phe Asn Phe Leu Arg Gln Ser Leu Asn Ser
 195 200 205
 Val Thr Gln Ala Gly Val Gln Trp Arg Asn Leu Gly Ser Leu Gln Pro
 210 215 220
 Leu Pro Pro Gly Phe Lys Leu Phe Ser Cys Pro Ser Leu Leu Ser Ser
 225 230 235 240
 Trp Asp Tyr Arg Arg Pro Pro Arg Leu Ala Asn Phe Phe Val Phe Leu
 245 250 255
 Val Glu Met Gly Phe Thr Met Phe Ala Arg Leu Ile Leu Ile Ser Gly
 260 265 270
 Pro Cys Asp Leu Pro Ala Ser Ala Ser Gln Ser Ala Gly Ile Thr Gly
 275 280 285
 Val Ser His His Ala Arg Leu Ile Phe Asn Phe Cys Leu Phe Glu Met
 290 295 300
 Glu Ser His Ser Val Thr Gln Ala Gly Val Gln Trp Pro Asn Leu Gly
 305 310 315 320
 Ser Leu Gln Pro Leu Pro Pro Gly Leu Lys Arg Phe Ser Cys Leu Ser
 325 330 335
 Leu Pro Ser Ser Trp Asp Tyr Gly His Leu Pro Pro His Pro Ala Asn
 340 345 350
 Phe Cys Ile Phe Ile Arg Gly Gly Val Ser Pro Tyr Leu Ser Gly Trp
 355 360 365
 Ser Gln Thr Pro Asp Leu Arg
 370 375

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1381 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCAGG CTGGAGTGCA ATGGCGCAAT	60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC	120
AGTAGCTGGG ATTACAGGCA TGTGCACCAC GCTCGGCTAA TTTTGTATTT TTTTGTAGTA	180

09964666-092801

GAGATGGAGT TTAACCTCCAT GTTGGTCAGG CTGGTCTCGA ACTCCCGACC TCAGATGATC	240
TCCCGTCTCG GCCTGCCCAA AGTGCTGAGA TTACAGGCAT GAGCCACCAT GCCCGGCCTC	300
TGCCTGGCTA ATTTTGTGG TAGAAACAGG GTTTCCTGA TGTGCCCCAA GCTGGTCTCC	360
TGAGCTCAAG CAGTCCACCT GCCTCAGCCT CCCAAAGTGC TGGGATTACA GCGTCAGCC	420
GTGCCTGGCC TTTTATTTT ATTTTTTTTA AGACACAGGT GTACCACTCT TACCCAGGAT	480
GAAGTGCACT GGTGTGATCA CAGCTCACTG CAGCCTTCAA CTCCTGAGAT CAAGCAATCC	540
TCCTGCCTCA GCCTCCCAAG TAGCTGGGAC CAAAGACATG CACCACTACA CCTGGTAATT	600
TTTATTTTTTA TTTTAAATTT TTTGAGACAG AGTCTCACTC TGTCACCCAG GCTGGAGTGC	660
AGTGGCGCAA TCTTGGCTCA CTGCAACCTC TGCCTCCCGG GTTCAAGTTA TTCTCCTGCC	720
CCAGCCTCCT GAGTAGCTGG GACTACAGGC GCCCACCACG CCTAGCTAAT TTTTTGTAT	780
TTTAGTAGA GATGGGGTTT CACCATGTTC GCCAGGTTGA TCTTGATCTC TTGACCTTGT	840
GATCTGCCTG CCTCGGCCTA CCCAAAGTGC TGGGATTACA GGTCGTGACT CCACGCCGGC	900
CTATTTTTTA TTTTGTGTTG TTTGAAATGG AATCTCACTC TGTTACCCAG GTCGGAGTGC	960
AATGGCAAAT CTCGGCTACT CGCAACCTCT GCCTCCCGGG TCAAGCGATT CTCCTGTCTC	1020
AGCCTCCCAA GCAGCTGGGA TTACGGGACC TGCACCACAC CCCGCTAATT TTTGTATTTT	1080
CATTAGAGGC GGGTTTACCA TATTTGTCAG GCTGGGTCTC AACTCCTGA CCTCAGGTGA	1140
CCCACCTGCC TCAGCCTTCC AAAGTGCTGG GATTACAGGC GTGAGCCACC TCACCCAGCC	1200
GGCTAATTTG GAATAAAAAA TATGTAGCAA TGGGGGTCTG CTATGTTGCC CAGGCTGGTC	1260
TCAAACCTCT GGCTTCAGTC AATCCTTCCA AATGAGCCAC AACACCCAGC CAGTCACATT	1320
TTTTAAACAG TTACATCTTT ATTTTAGTAT ACTAGAAAGT AATAACAATA ACATGTCAAA	1380
C	1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

09564666-092801

TTTTTTTTTTT GAGATGGAGT TTTCGCTCTT GTTGCCCAGG CTGGAGTGCA ATGGCGCAAT	60
CTCAGCTCAC CGCAACCTCC GCCTCCCGGG TTCAAGCGAT TCTCCTGCCT CAGCCTCCCC	120
AGTAGGCTGG GATTACAGGC ATGTGCACCA CGCTCGGCTA ATTTTGTATT TTTTTTTAGT	180
AGAGATGGAG TTTCTCCATG TTGGTCAGGC TGGTCTCGAA CTCCGACCTC AGATGATCCT	240
CCCGTCTCGG CCTCCCAAAG TGCTAGATAC AGGACTGAGC ACCATGCCCC GCCTCTGCCT	300
GGCTAATTTT TGTGGTAGAA ACAGGGTTTC ACTGATGTGC CCAAGCTGGT CTCCTGAGCT	360
CAAGCAGTCC ACCTGCCTCA GCCTCCCAA GTGCTGGGAT TACAGGCGTG CAGCCGTGCC	420
TGGCCTTTTT ATTTTATTTT TTTTAAGACA CAGGTGTCCC ACTCTTACCC AGGATGAAGT	480
GCAGTGGTGT GATCACAGCT CACTGCAGCC TTCAACTCTG AGATCAAGCA TCCTCCTGCC	540
TCAGCCTCCC AAAGTAGCTG GGACCAAAGA CATGCACCAC TACACCTGGC TAATTTTTAT	600
TTTTATTTTT AATTTTTTTGA GACAGAGTCT CAACTCTGTC ACCCAGGCTG GAGTGCAGTG	660
GCGCAATCTT GGCTCACTGC AACCTCTGCC TCCCGGGTTC AAGTTATTCT CCTGCCCCAG	720
CCTCCTGAGT AGCTGGGACT ACAGGCGCCC ACCACGCCTA GCTAATTTTT TTGTATTTTT	780
AGTAGAGATG GGGTTTCACC ATGTTGCGCA GGTGATGCT AGATCTCTTG ACCTTGTGAT	840
CTGCCTGCCT CGGCCTCCCA AAGTGCTGGG ATTACAGGAC GTGACGCCCA CCGCCCGGCC	900
TATTTTTAAT TTTTGTTTGT TTGAAATGGA ATCTCACTCT GTTACCCAGG CTGGAGTGCA	960
ATGGCCAAAT CTCGGCTCAC TGCAACCTCT GCCTCCCGGG CTCAAGCGAT TCTCCTGTCT	1020
CAGCCTCCCA AGCAGCTGGG ATTACGGGCA CCTGCACCAC ACCCGCTAA TTTTGTATT	1080
TTCATTAGAG GCGGGGTTTC ACCATATTTG TCAGGCTGGT CTCAAACCTC TGACCTCAGG	1140
TGACCCACCT GCCTCAGCCT TCCAAAGTGC TGGGATTACA GCGGTGACGC CTCACCCAGC	1200
CGGCTAATTT AGATAAAAAA ATATGTAGCA ATGGGGGGTC TTGCTATGTT GCCCAGGCTG	1260
GTCTCAAAC TCTGGCTTCA TGCAATCCTT CCAAATGAGC CACAACACC AGCCAGTCAC	1320
ATTTTTAAAC AGTTACATCT TTATTTTAGT ATACTAGAAA GTGATACGAT AACATGGCGG	1380
AACCTGCAAA TTCGAGTAGT ACAGAGTCTT TTATAACT	1418

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

09964656-092801

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 24 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 20 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 19 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

09964666-092801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

09964656-092801

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14

09964666-092801

Applicant's or agent's file
reference number 0609.437PC01

International application
TBA

INDICATIONS RELATING TO A DEPOSITED MICROORGANISM
(PCT Rule 13bis)

A. The indications made below relate to the microorganism referred to in the description on page 5, line 11.

B. IDENTIFICATION OF DEPOSIT

Further deposits are identified on an additional sheet ☐

Name of depositary institution
AMERICAN TYPE CULTURE COLLECTION

Address of depositary institution (including postal code and country)

12301 Parklawn Drive
Rockville, Maryland 20852
United States of America

Date of deposit
March 16, 1993

Accession Number
69262

C. ADDITIONAL INDICATIONS (leave blank if not applicable)

This information is continued on an additional sheet ☐

Escherichia coli: AD10-7-DH1

D. DESIGNATED STATES FOR WHICH INDICATIONS ARE MADE (if the indications are not for all designated States)

E. SEPARATE FURNISHING OF INDICATIONS (leave blank if not applicable)

The indications listed below will be submitted to the international Bureau later (specify the general nature of the indications, e.g., "Accession Number of Deposit")

For receiving Office use only

☐ This sheet was received with the international application

Authorized officer

For International Bureau use only

☐ This sheet was received by the International Bureau on:

Authorized officer

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: de la Monte, Suzanne
Wands, Jack R.
- (ii) TITLE OF INVENTION: Transgenic Animals and Cell Lines for
Screening Drugs Effective for the Treatment or Prevention
of Alzheimer's Disease
- (iii) NUMBER OF SEQUENCES: 14
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
 - (B) STREET: 1100 New York Ave., Suite 600
 - (C) CITY: Washington
 - (D) STATE: DC
 - (E) COUNTRY: USA
 - (F) ZIP: 20005-3934
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Esmond, Robert W.
 - (B) REGISTRATION NUMBER: 32,893
 - (C) REFERENCE/DOCKET NUMBER: 0609.4370000
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-371-2600
 - (B) TELEFAX: 202-371-2540

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: both
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 15..1139
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT TGAG ATG GAG TTT TCG CTC TTG TTG CCC AGG CTG GAG TGC
 Met Glu Phe Ser Leu Leu Leu Pro Arg Leu Glu Cys
 1 5 10

50

09964666-092801

AAT	GGC	GCA	ATC	TCA	GCT	CAC	CGC	AAC	CTC	CGC	CTC	CCG	GGT	TCA	AGC	98
Asn	Gly	Ala	Ile	Ser	Ala	His	Arg	Asn	Leu	Arg	Leu	Pro	Gly	Ser	Ser	
		15					20					25				
GAT	TCT	CCT	GCC	TCA	GCC	TCC	CCA	GTA	GCT	GGG	ATT	ACA	GGC	ATG	TGC	146
Asp	Ser	Pro	Ala	Ser	Ala	Ser	Pro	Val	Ala	Gly	Ile	Thr	Gly	Met	Cys	
	30					35					40					
ACC	CAC	GCT	CGG	CTA	ATT	TTG	TAT	TTT	TTT	TTA	GTA	GAG	ATG	GAG	TTT	194
Thr	His	Ala	Arg	Leu	Ile	Leu	Tyr	Phe	Phe	Leu	Val	Glu	Met	Glu	Phe	
	45				50					55					60	
CTC	CAT	GTT	GGT	CAG	GCT	GGT	CTC	GAA	CTC	CCG	ACC	TCA	GAT	GAT	CCC	242
Leu	His	Val	Gly	Gln	Ala	Gly	Leu	Glu	Leu	Pro	Thr	Ser	Asp	Asp	Pro	
				65					70					75		
TCC	GTC	TCG	GCC	TCC	CAA	AGT	GCT	AGA	TAC	AGG	ACT	GGC	CAC	CAT	GCC	290
Ser	Val	Ser	Ala	Ser	Gln	Ser	Ala	Arg	Tyr	Arg	Thr	Gly	His	His	Ala	
			80					85					90			
CGG	CTC	TGC	CTG	GCT	AAT	TTT	TGT	GGT	AGA	AAC	AGG	GTT	TCA	CTG	ATG	338
Arg	Leu	Cys	Leu	Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met	
		95					100					105				
TGC	CCA	AGC	TGG	TCT	CCT	GAG	CTC	AAG	CAG	TCC	ACC	TGC	CTC	AGC	CTC	386
Cys	Pro	Ser	Trp	Ser	Pro	Glu	Leu	Lys	Gln	Ser	Thr	Cys	Leu	Ser	Leu	
	110					115					120					
CCA	AAG	TGC	TGG	GAT	TAC	AGG	CGT	GCA	GCC	GTG	CCT	GGC	CTT	TTT	ATT	434
Pro	Lys	Cys	Trp	Asp	Tyr	Arg	Arg	Ala	Ala	Val	Pro	Gly	Leu	Phe	Ile	
	125				130					135					140	
TTA	TTT	TTT	TTA	AGA	CAC	AGG	TGT	CCC	ACT	CTT	ACC	CAG	GAT	GAA	GTG	482
Leu	Phe	Phe	Leu	Arg	His	Arg	Cys	Pro	Thr	Leu	Thr	Gln	Asp	Glu	Val	
				145					150					155		
CAG	TGG	TGT	GAT	CAC	AGC	TCA	CTG	CAG	CCT	TCA	ACT	CCT	GAG	ATC	AAG	530
Gln	Trp	Cys	Asp	His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	
			160					165					170			
CAT	CCT	CCT	GCC	TCA	GCC	TCC	CAA	GTA	GCT	GGG	ACC	AAA	GAC	ATG	CAC	578
His	Pro	Pro	Ala	Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr	Lys	Asp	Met	His	
		175					180					185				
CAC	TAC	ACC	TGG	CTA	ATT	TTT	ATT	TTT	ATT	TTT	AAT	TTT	TTG	AGA	CAG	626
His	Tyr	Thr	Trp	Leu	Ile	Phe	Ile	Phe	Ile	Phe	Asn	Phe	Leu	Arg	Gln	
	190					195					200					
AGT	CTC	AAC	TCT	GTC	ACC	CAG	GCT	GGA	GTG	CAG	TGG	CGC	AAT	CTT	GGC	674
Ser	Leu	Asn	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Arg	Asn	Leu	Gly	
	205				210					215					220	
TCA	CTG	CAA	CCT	CTG	CCT	CCC	GGG	TTC	AAG	TTA	TTC	TCC	TGC	CCC	AGC	722
Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Phe	Lys	Leu	Phe	Ser	Cys	Pro	Ser	
				225					230					235		
CTC	CTG	AGT	AGC	TGG	GAC	TAC	AGG	CGC	CCA	CCA	CGC	CTA	GCT	AAT	TTT	770
Leu	Leu	Ser	Ser	Trp	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu	Ala	Asn	Phe	
				240				245					250			
TTT	GTA	TTT	TTA	GTA	GAG	ATG	GGG	TTC	ACC	ATG	TTC	GCC	AGG	TTG	ATC	818
Phe	Val	Phe	Leu	Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arg	Leu	Ile	
		255					260					265				
TTG	ATC	TCT	GGA	CCT	TGT	GAT	CTG	CCT	GCC	TCG	GCC	TCC	CAA	AGT	GCT	866

Leu	Ile	Ser	Gly	Pro	Cys	Asp	Leu	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala		
270						275					280						
GGG	ATT	ACA	GGC	GTG	AGC	CAC	CAC	GCC	CGG	CTT	ATT	TTT	AAT	TTT	TGT		914
Gly	Ile	Thr	Gly	Val	Ser	His	His	Ala	Arg	Leu	Ile	Phe	Asn	Phe	Cys		
285					290				295						300		
TTG	TTT	GAA	ATG	GAA	TCT	CAC	TCT	GTT	ACC	CAG	GCT	GGA	GTG	CAA	TGG		962
Leu	Phe	Glu	Met	Glu	Ser	His	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp		
				305					310					315			
CCA	AAT	CTC	GGC	TCA	CTG	CAA	CCT	CTG	CCT	CCC	GGG	CTC	AAG	CGA	TTC		1010
Pro	Asn	Leu	Gly	Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu	Lys	Arg	Phe		
			320					325					330				
TCC	TGT	CTC	AGC	CTC	CCA	AGC	AGC	TGG	GAT	TAC	GGG	CAC	CTG	CCA	CCA		1058
Ser	Cys	Leu	Ser	Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Gly	His	Leu	Pro	Pro		
		335					340					345					
CAC	CCC	GCT	AAT	TTT	TGT	ATT	TTC	ATT	AGA	GGC	GGG	GTT	TCA	CCA	TAT		1106
His	Pro	Ala	Asn	Phe	Cys	Ile	Phe	Ile	Arg	Gly	Gly	Val	Ser	Pro	Tyr		
	350					355					360						
TTG	TCA	GGC	TGG	TCT	CAA	ACT	CCT	GAC	CTC	AGG	TGACCCACCT	GCCTCAGCCT					1159
Leu	Ser	Gly	Trp	Ser	Gln	Thr	Pro	Asp	Leu	Arg							
365					370				375								
TCCAAAGTGC	TGGGATTACA	GGCGTGAGCC	ACCTCACCCA	GCCGGCTAAT	TTAGATAAAA												1219
AAATATGTAG	CAATGGGGGG	TCTTGCTATG	TTGCCCAGGC	TGGTCTCAAA	CTTCTGGCTT												1279
CATGCAATCC	TTCCAAATGA	GCCACAACAC	CCAGCCAGTC	ACATTTTSTA	AACAGTTACA												1339
TCTTTATTTT	AGTATACTAG	AAAGTAATAC	AATAAACATG	TCAAACCTGC	AAATTCAGTA												1399
GTAACAGAGT	TCTTTTATAA	CTTTTAAACA	AAGCTTTAGA	GCA													1442

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 375 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Glu	Phe	Ser	Leu	Leu	Leu	Pro	Arg	Leu	Glu	Cys	Asn	Gly	Ala	Ile		
1				5					10					15			
Ser	Ala	His	Arg	Asn	Leu	Arg	Leu	Pro	Gly	Ser	Ser	Asp	Ser	Pro	Ala		
		20					25						30				
Ser	Ala	Ser	Pro	Val	Ala	Gly	Ile	Thr	Gly	Met	Cys	Thr	His	Ala	Arg		
		35				40					45						
Leu	Ile	Leu	Tyr	Phe	Phe	Leu	Val	Glu	Met	Glu	Phe	Leu	His	Val	Gly		
	50					55				60							
Gln	Ala	Gly	Leu	Glu	Leu	Pro	Thr	Ser	Asp	Asp	Pro	Ser	Val	Ser	Ala		
	65				70				75						80		
Ser	Gln	Ser	Ala	Arg	Tyr	Arg	Thr	Gly	His	His	Ala	Arg	Leu	Cys	Leu		

85					90					95					
Ala	Asn	Phe	Cys	Gly	Arg	Asn	Arg	Val	Ser	Leu	Met	Cys	Pro	Ser	Trp
			100					105					110		
Ser	Pro	Glu	Leu	Lys	Gln	Ser	Thr	Cys	Leu	Ser	Leu	Pro	Lys	Cys	Trp
		115					120					125			
Asp	Tyr	Arg	Arg	Ala	Ala	Val	Pro	Gly	Leu	Phe	Ile	Leu	Phe	Phe	Leu
	130					135					140				
Arg	His	Arg	Cys	Pro	Thr	Leu	Thr	Gln	Asp	Glu	Val	Gln	Trp	Cys	Asp
	145					150					155				160
His	Ser	Ser	Leu	Gln	Pro	Ser	Thr	Pro	Glu	Ile	Lys	His	Pro	Pro	Ala
				165					170					175	
Ser	Ala	Ser	Gln	Val	Ala	Gly	Thr	Lys	Asp	Met	His	His	Tyr	Thr	Trp
			180					185					190		
Leu	Ile	Phe	Ile	Phe	Ile	Phe	Asn	Phe	Leu	Arg	Gln	Ser	Leu	Asn	Ser
		195					200					205			
Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Arg	Asn	Leu	Gly	Ser	Leu	Gln	Pro
	210					215					220				
Leu	Pro	Pro	Gly	Phe	Lys	Leu	Phe	Ser	Cys	Pro	Ser	Leu	Leu	Ser	Ser
	225					230					235				240
Trp	Asp	Tyr	Arg	Arg	Pro	Pro	Arg	Leu	Ala	Asn	Phe	Phe	Val	Phe	Leu
				245					250					255	
Val	Glu	Met	Gly	Phe	Thr	Met	Phe	Ala	Arg	Leu	Ile	Leu	Ile	Ser	Gly
			260					265					270		
Pro	Cys	Asp	Leu	Pro	Ala	Ser	Ala	Ser	Gln	Ser	Ala	Gly	Ile	Thr	Gly
		275					280					285			
Val	Ser	His	His	Ala	Arg	Leu	Ile	Phe	Asn	Phe	Cys	Leu	Phe	Glu	Met
	290					295					300				
Glu	Ser	His	Ser	Val	Thr	Gln	Ala	Gly	Val	Gln	Trp	Pro	Asn	Leu	Gly
	305					310					315				320
Ser	Leu	Gln	Pro	Leu	Pro	Pro	Gly	Leu	Lys	Arg	Phe	Ser	Cys	Leu	Ser
				325					330					335	
Leu	Pro	Ser	Ser	Trp	Asp	Tyr	Gly	His	Leu	Pro	Pro	His	Pro	Ala	Asn
			340					345					350		
Phe	Cys	Ile	Phe	Ile	Arg	Gly	Gly	Val	Ser	Pro	Tyr	Leu	Ser	Gly	Trp
		355					360					365			
Ser	Gln	Thr	Pro	Asp	Leu	Arg									
	370				375										

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1381 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TTTTTTTTTTT	GAGATGGAGT	TTTCGCTCTT	GTTGCCCAGG	CTGGAGTGCA	ATGGCGCAAT	60
CTCAGCTCAC	CGCAACCTCC	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
AGTAGCTGGG	ATTACAGGCA	TGTGCACCAC	GCTCGGCTAA	TTTTGTATTT	TTTTTTAGTA	180
GAGATGGAGT	TTAACTCCAT	GTTGGTCAGG	CTGGTCTCGA	ACTCCCGACC	TCAGATGATC	240
TCCCGTCTCG	GCCTGCCCAA	AGTGCTGAGA	TTACAGGCAT	GAGCCACCAT	GCCCGGCCTC	300
TGCCTGGCTA	ATTTTTGTGG	TAGAAACAGG	GTTTCACTGA	TGTTGCCCAA	GCTGGTCTCC	360
TGAGCTCAAG	CAGTCCACCT	GCCTCAGCCT	CCCAAAGTGC	TGGGATTACA	GGCGTCAGCC	420
GTGCCTGGCC	TTTTTATTTT	ATTTTTTTTA	AGACACAGGT	GTACCACTCT	TACCCAGGAT	480
GAAGTGCAGT	GGTGTGATCA	CAGCTCACTG	CAGCCTTCAA	CTCCTGAGAT	CAAGCAATCC	540
TCCTGCCTCA	GCCTCCCAAG	TAGCTGGGAC	CAAAGACATG	CACCACTACA	CCTGGTAATT	600
TTTATTTTTTA	TTTTTAATTT	TTTGAGACAG	AGTCTCACTC	TGTCACCCAG	GCTGGAGTGC	660
AGTGGCGCAA	TCTTGGCTCA	CTGCAACCTC	TGCCTCCCGG	GTTCAAGTTA	TTCTCCTGCC	720
CCAGCCTCCT	GAGTAGCTGG	GACTACAGGC	GCCCACCACG	CCTAGCTAAT	TTTTTTGTAT	780
TTTTAGTAGA	GATGGGGTTT	CACCATGTTC	GCCAGGTTGA	TCTTGATCTC	TTGACCTTGT	840
GATCTGCCTG	CCTCGGCCTA	CCCAAAGTGC	TGGGATTACA	GGTCGTGACT	CCACGCCGGC	900
CTATTTTTTAA	TTTTTGTTTG	TTTGAAATGG	AATCTCACTC	TGTTACCCAG	GTCGGAGTGC	960
AATGGCAAAT	CTCGGCTACT	CGCAACCTCT	GCCTCCCGGG	TCAAGCGATT	CTCCTGTCTC	1020
AGCCTCCCAA	GCAGCTGGGA	TTACGGGACC	TGCACCACAC	CCCCTAATT	TTTGTATTTT	1080
CATTAGAGGC	GGGTTTACCA	TATTTGTCAG	GCTGGGTCTC	AAACTCCTGA	CCTCAGGTGA	1140
CCCACCTGCC	TCAGCCTTCC	AAAGTGCTGG	GATTACAGGC	GTGAGCCACC	TCACCCAGCC	1200
GGCTAATTTG	GAATAAAAAA	TATGTAGCAA	TGGGGGTCTG	CTATGTTGCC	CAGGCTGGTC	1260
TCAAACCTTCT	GGCTTCAGTC	AATCCTTCCA	AATGAGCCAC	AACACCCAGC	CAGTCACATT	1320
TTTTAAACAG	TTACATCTTT	ATTTTAGTAT	ACTAGAAAGT	AATACAATAA	ACATGTCAAA	1380
C						1381

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1418 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: both
- (D) TOPOLOGY: both

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTTTTTTTTTT	GAGATGGAGT	TTTCGCTCTT	GTTGCCCAGG	CTGGAGTGCA	ATGGCGCAAT	60
CTCAGCTCAC	CGCAACCTCC	GCCTCCCGGG	TTCAAGCGAT	TCTCCTGCCT	CAGCCTCCCC	120
AGTAGGCTGG	GATTACAGGC	ATGTGCACCA	CGCTCGGCTA	ATTTTGTATT	TTTTTTTAGT	180
AGAGATGGAG	TTTCTCCATG	TTGGTCAGGC	TGGTCTCGAA	CTCCGACCTC	AGATGATCCT	240
CCCGTCTCGG	CCTCCCAAAG	TGCTAGATAC	AGGACTGAGC	ACCATGCCCC	GCCTCTGCCT	300
GGCTAATTTT	TGTGGTAGAA	ACAGGGTTTC	ACTGATGTGC	CCAAGCTGGT	CTCCTGAGCT	360
CAAGCAGTCC	ACCTGCCTCA	GCCTCCCAA	GTGCTGGGAT	TACAGGCGTG	CAGCCGTGCC	420
TGGCCTTTTT	ATTTTATTTT	TTTAAAGACA	CAGGTGTCCC	ACTCTTACCC	AGGATGAAGT	480
GCAGTGGTGT	GATCACAGCT	CACTGCAGCC	TTCAACTCTG	AGATCAAGCA	TCCTCCTGCC	540
TCAGCCTCCC	AAAGTAGCTG	GGACCAAAGA	CATGCACCAC	TACACCTGGC	TAATTTTTAT	600
TTTTATTTTT	AATTTTTTGA	GACAGAGTCT	CAACTCTGTC	ACCCAGGCTG	GAGTGCAGTG	660
GCGCAATCTT	GGCTCACTGC	AACCTCTGCC	TCCCGGGTTC	AAGTTATTCT	CCTGCCCCAG	720
CCTCCTGAGT	AGCTGGGACT	ACAGGCGCCC	ACCACGCCTA	GCTAATTTTT	TTGTATTTTT	780
AGTAGAGATG	GGGTTTCACC	ATGTTCGCCA	GGTTGATGCT	AGATCTCTTG	ACCTTGTGAT	840
CTGCCTGCCT	CGGCCTCCCA	AAGTGCTGGG	ATTACAGGAC	GTGACGCCCA	CCGCCCCGGC	900
TATTTTTAAT	TTTGTTTTGT	TTGAAATGGA	ATCTCACTCT	GTTACCCAGG	CTGGAGTGCA	960
ATGGCCAAAT	CTCGGCTCAC	TGCAACCTCT	GCCTCCCGGG	CTCAAGCGAT	TCTCCTGTCT	1020
CAGCCTCCCA	AGCAGCTGGG	ATTACGGGCA	CCTGCACCAC	ACCCCGCTAA	TTTTTGTATT	1080
TTCATTAGAG	GCGGGGTTTC	ACCATATTTG	TCAGGCTGGT	CTCAAACTCC	TGACCTCAGG	1140
TGACCCACCT	GCCTCAGCCT	TCCAAAGTGC	TGGGATTACA	GGCGTGACGC	CTCACCAGC	1200
CGGCTAATTT	AGATAAAAAA	ATATGTAGCA	ATGGGGGGTC	TTGCTATGTT	GCCCAGGCTG	1260
GTCTCAAACT	TCTGGCTTCA	TGCAATCCTT	CCAAATGAGC	CACAACACCC	AGCCAGTCAC	1320
ATTTTTTAAAC	AGTTACATCT	TTATTTTAGT	ATACTAGAAA	GTGATACGAT	AACATGGCGG	1380
AACCTGCAAA	TTGAGTAGT	ACAGAGTCTT	TTATAACT			1418

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TGTCCCACTC TTACCCAGGA TG

22

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AAGCAGGCAG ATCACAAGGT CCAG

24

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AATGGATGAC GATATCGCTG

20

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

ATGAGGTAGT CTGTCAGGT

19

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

0996466-092801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

TTTCATCCTGG GTAAGAGTGG GACACCTGTG

30

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

TGGTGCATGT CTTTGGTCCC AGCTAC

26

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

ATCAACCTGG CGAACATGGT GAACCCCATC

30

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CACTGCACTT NCCA

14

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

0954665-092801

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CCAGGTGTAG NCCA

14

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CAAGGTCCAG NCCA

14

09564566-092801
108260" 99949560